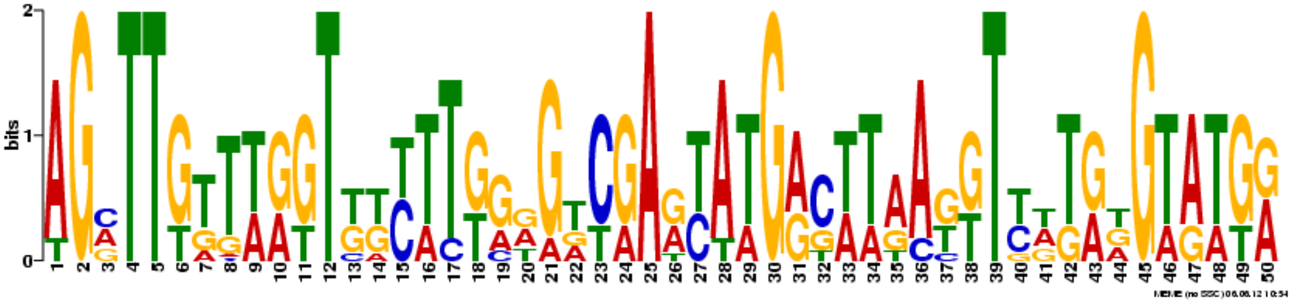
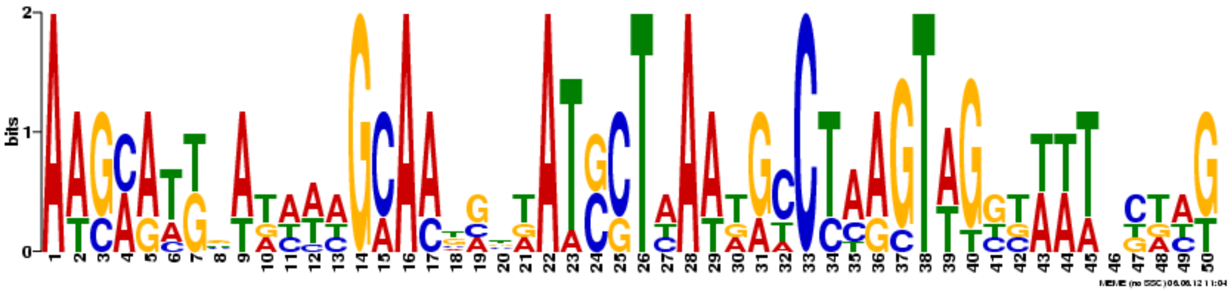
Figure S1: Motifs identified by Meme Analysis

Motif 1:



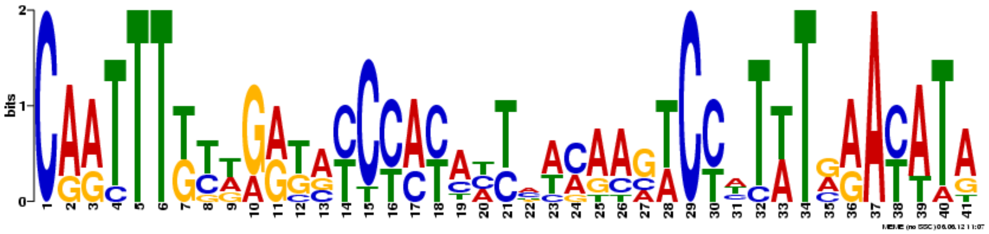
Name	Strand	Start	*p*-value	Sites		
bp2N	+	249	2.79e-22	AGCAAGAAGA	AGCTTGGTTAGTGTTTTGGAGTCGAATATGACTTGATGTCATGTGTATGA	TTGAGTATAA
bp2N	+	81	4.79e-21	AGCTAGAAGA	AGCTTGGNTAGTGTTTTGGAGTCGAATATGACTTGATGTCATGTGTATGA	TTGAGTATAA
bp11N	+	288	2.05e-19	AGATTAAGGC	AGGTTGTTAGGTTGCATTGTGACGAGTATGGCTAAAGTTTTTAAGTAAGG	GTCTATCATC
bp2N	+	426	2.27e-19	AGCAAGAAGA	AGCTTGATTAGTGTTTTGGAGTTGAATATGACTTTATGTCATGTGTATGA	TTGAGTATAA
bp5N	-	309	2.80e-19	AGATTAAGGC	AGGTTGTTAGGTTGCATTGTGACGAGTATGGCTAACGGTTTTAAGTAAGG	GTCTATCACT
bp11N	+	446	1.90e-17	CTTCAACTTA	AGATTTTTTGTTTGCTTGAGGGCAAGCAAGAGATAAGTTTGGGGGAGTTG	ATAACACAGT
bp5N	-	151	8.00e-16	TTTCAACTTA	AGATTTTTTGTTTACTCGAGGGCAATCAAGAGATAAGTTTGGGGGAGTTG	ATAACACTGT
bp5N	-	1012	2.54e-15	CATTTGTGTG	TGATTGTGAGGTCTTTTTCGATTGAGCTTGGTATAACGTGTTAGGTATGA	GCCGACAAGA

Motif 2:



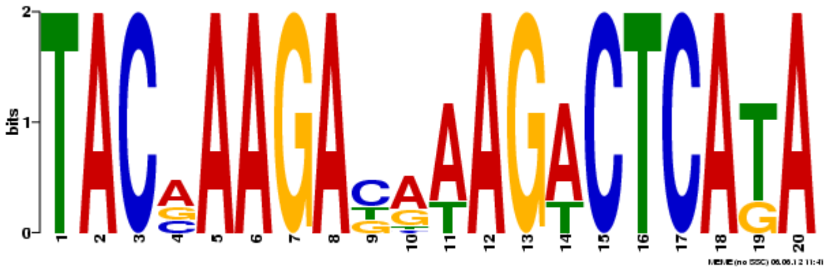
Name	Strand	Start	*p*-value	Sites		
bp2N	+	484	2.34e-18	GATTGAGTAT	AAGAATTTAAATCGCAATCTTATCCTAAAAGCCTAAGTAGTGTTTCCTTG	TTAGAATATA
bp11N	-	355	5.51e-18	TCAAAAACCG	AAGCATGCATATAGAACGGGTATGCTCAATGTCCTGGTAGCTAATTCTAG	GTTGCAAGAT
bp5N	+	242	7.39e-17	TCAAAAATCG	AAGCATGCATATAGAACAGGTAAGCTCAATGTCCAGGTAGCTAATTCTAG	GTTGCAAAGT
bp2N	+	139	1.31e-16	GATTGAGTAT	AAGAACTTAAACCGCAACCATATCCTAAAAGCCTAAGTAGTGTTTCCTTG	TTAGAATATA
bp11N	-	180	2.67e-16	ATTAAGCACG	AACAGTGGATCAAGCAATGCAATGGTTATGACCTCAGTTGGTTTTGGGCT	TAGGCTAAGA
bp11N	-	589	1.05e-15	ACACCAAAAG	ATGCAATATGTATGCAAGATGATCCTAAATGCCTAAGTTGGCAAAATAAG	CTAAATGTGA
bp5N	+	9	1.42e-15	CACCAAAAA	ATGCAATGTGTATGCAAGATGATCCTAAATGCCTAAGTATGCAAAATAAG	CTAAAATGGT
bp5N	+	380	8.68e-15	TTTAAGCACG	AACAGTGGATCAAGCAATGCAATGGTTATGAACTCACTTGGTTTTGGGCT	TAGGCTAAGA

Motif 3:



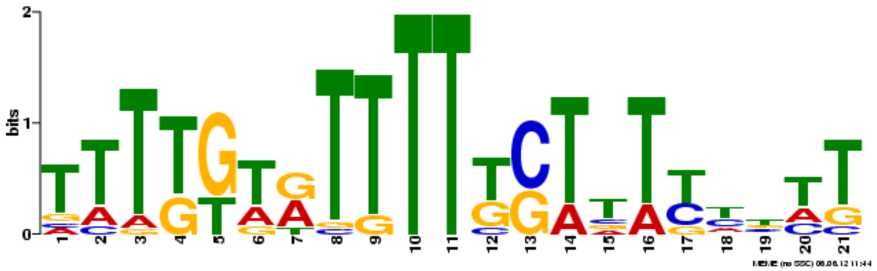
Name	**Strand**	**Start**	***p*-value**		**Sites**	
bp1N	+	81	3.95e-16	AAATAACAAA	CAATTTTTTGGTGTCCATAATAACAAGTCCWTTTAAATATA	TCCATTCGGA
bp1N	+	280	6.85e-16	AATCATCAAA	CAATTTTTTGGCATCCATAATAACAAGTCCATTTAAATATA	TCCATTCAGA
bp1N	-	223	1.69e-15	GATTTTCTTT	CAGCTTGCAGAGACCTCCACCXTCAAGACCTTATGGACATG	GAACTCTGGT
bp1N	+	481	2.74e-15	AATCAACAAA	CAATTTGTTGGTGTCCATAATAACGAATCCATTTAAATATA	TCAATTCGGA
bp1N	-	422	4.82e-14	TTTTTTTTTT	CAATTTGCAGAGACTTCCACCCTCAAAACCXTATGGATATG	GAACTTTGGT
bp1N	-	23	1.20e-13	TTTTTTTTTA	CAGTTTGCAGAGACCTCCXCCTCGGAGACTTTATGGACATA	GAAATTATAC
bp5N	-	201	1.30e-13	ATGCATGCTT	CGATTTTTGAATCCCCACCTTCAAACCTCTCTTTCAACTTA	AGATTTTTTG
bp11N	+	405	4.66e-13	ATGCATGCTT	CGGTTTTTGAATCCCCACCTTCAAACCTCTCCTTCAACTTA	AGATTTTTTG
bp1S	-	233	4.11e-12	CTTCTATTTC	CAATTTTGTGGTATCCATTTTGTATTGTCCATATGAACAAT	GTACTTTTGC

Motif 4:



Name	**Strand**	**Start**	***p*-value**	**Sites**
bp2N	+	542	1.10e-11	TGTTAGAATA TACGAAGACAAAGACTCATA TGGACTTCGG
bp2N	+	18	3.42e-11	GTTAGAAGGC TACAAAGACNAAGACTCATA TGGACCNTTG
bp2N	+	364	7.62e-11	CGTTAGAAGA TACAAAGATAAAGACTCATA TGGACTTCGG
bp2S	+	1076	3.89e-10	GAGGGAATCA TACCAAGAGGTAGTCTCAGA CCAGCATTAT

Motif 5:



Name	Strand	Start	*p*-value	Sites		
bp1S	-	71	1.44e-08	AATTTAATAA	TTTTGGGTTTTGCTTATCCTT	ATAAATCATA
bp1S	-	187	3.26e-08	TGGTGACCAT	TTTTGTATGTTGGTTTCCTCT	TTTGTACCCA
bp1N	-	877	1.03e-07	ATTTTGATGG	TATGGAATTTTTCTTTCACTT	AGGGGATTGG
bp1S	+	1294	1.53e-07	AATCAAAATA	TTTTGTATTTTTCAATTTGTT	AGAGATAAAA
bp11S	+	1666	1.74e-07	TTGTGCTCTG	TTTTGTGGTTTTGTTTCATTT	TTAGCTTAAT
bp3N	-	609	3.97e-07	TTCCATCTTT	GCTTGTGTTTTGCTTTTCTCC	AGCCTAGATA
bp3N	-	249	3.97e-07	ACCTTGTCGC	TTTGTGGTTTTTCATTCACTT	GGGCCTTAAA
bp5N	-	1712	8.31e-07	ATACCATTGG	CTTTTTATTTTTCTTTGTGTG	TTTTGTGTTT
bp3S	+	87	8.31e-07	CAATAGAAAA	TTTTGAGTTTTGGATACTCCG	GGTTTACCCG
bp5N	+	1558	1.01e-06	TCAAATTTTT	TATGGTTTTTTTCTATGCCTT	AGATTGATGC
bp5N	-	1691	1.11e-06	TCTTTGTGTG	TTTTGTGTTTTGGTCTTGAAT	TTTTCCTCAG
bp11S	-	976	1.23e-06	TGATATATGA	TATTGTATTTTCCTGTTTGAG	TATATTTTCC
bp11S	+	1168	2.10e-06	ATATGATTAT	TTTGTTGTTTTTGTGATATAT	ATTGTATTTA
bp5S	+	1345	2.10e-06	TTCTCTTCTT	TTATGTACTTTGGTTTTTGTT	ATTCGAAAGA
bp5S	-	1196	2.28e-06	ATATTAAGAA	GTTGGGGTTTTCCTCATTGAT	CACCAAAATG
bp3S	+	1255	2.28e-06	AAATTTCAAT	TTGGTAATTTTTGTTTTTGTT	TGAATTTACA
bp11N	+	1085	2.70e-06	TAGCTTTTAT	CCTTTAGTTTTTCTTTGTGTT	CTTGAATCTT
bp1S	+	1498	3.17e-06	TCCATCCAAA	TATTTTGTTTTTGTCATATCT	TAATATGTAA
bp11S	+	1746	3.43e-06	TGCATAGAAG	GTATGAATTTTTCTTTTCTAG	ATATATAAGG
bp2S	-	365	3.71e-06	TCCGTCGTGG	ATTGGTATGTTTCAGTCCTCT	CTACTATATA
bp1S	-	1351	3.71e-06	TGTTAAAGTA	TTTTGTATTTTTCAATTAATG	GCATTCGATT
bp5S	-	1239	4.99e-06	ATTCTAAGGG	TATGTTTTGTTGGTTTCCTAT	TTATATCTTT
bp1N	-	638	4.99e-06	TGGCGGCTTG	ATTTGATTTTTGCTCTCTCTC	ATGTGTCAAA